
PPSRAH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 17 08:30:37 1995; MasPar time 12.94 Seconds
Tabular output not generated. 585.410 Million cell updates/sec

Title: >US-08-380-051-2

Description: (1:494) from US08380051.pep

Perfect Score: 3614

Sequence: 1 MIKLIVFLKRESAFNEWTM.....KTETDMSLHPLQETKYDLY 494

Scoring table: PAM 150

Gap 11

Searched: 43470 seqs, 15335248 residues

Database:

swiss-prot31
1 part1
2 part2
3 part3
4 part4
5 part5
6 part6
7 part7
8 part8

Statistics: Mean 52.508; Variance 112.681; scale 0.466

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3433	95.0	475	6	PPAT_HUMAN PEROXISOME PROLIFERAT	0.00e+00
2	3311	91.6	470	6	PPAT_MOUSE PEROXISOME PROLIFERAT	0.00e+00
3	2579	71.4	477	6	PPAT_XENLA PEROXISOME PROLIFERAT	0.00e+00
4	1946	53.8	468	6	PPAR_HUMAN PEROXISOME PROLIFERAT	0.00e+00
5	1932	53.5	468	6	PPAR_MOUSE PEROXISOME PROLIFERAT	0.00e+00
6	1930	53.4	468	6	PPAR_RAT PEROXISOME PROLIFERAT	0.00e+00
7	1921	53.2	441	6	PPAS_HUMAN PEROXISOME PROLIFERAT	0.00e+00
8	1894	52.4	474	6	PPAR_XENLA PEROXISOME PROLIFERAT	0.00e+00
9	1886	52.2	440	6	PPAS_MOUSE PEROXISOME PROLIFERAT	0.00e+00
10	1743	48.2	396	6	PPAS_XENLA PEROXISOME PROLIFERAT	1.37e-303

11	706	19.5	1237	2	E75A_DROME	ECDYSONE-INDUCIBLE PR	6.45e-103
12	641	17.7	1443	2	E75C_DROME	ECDYSONE-INDUCIBLE PR	9.62e-91
13	558	15.4	158	6	PPAU_MOUSE	PEROXISOME PROLIFERAT	2.36e-75
14	528	14.6	1394	2	E75B_DROME	ECDYSONE-INDUCIBLE PR	7.64e-70
15	525	14.5	369	7	THB1_XENLA	THYROID HORMONE RECP	2.71e-69
16	525	14.5	373	7	THB5_XENLA	THYROID HORMONE RECP	2.71e-69
17	518	14.3	369	7	THB_CHICK	THYROID HORMONE RECP	5.16e-68
18	518	14.3	476	7	THB2_HUMAN	THYROID HORMONE RECP	5.16e-68
19	517	14.3	410	7	THA1_MOUSE	THYROID HORMONE RECP	7.86e-68
20	516	14.3	410	7	THA1_HUMAN	THYROID HORMONE RECP	1.20e-67
21	514	14.2	461	7	THB1_MOUSE	THYROID HORMONE RECP	2.78e-67
22	514	14.2	475	7	THB2_MOUSE	THYROID HORMONE RECP	2.78e-67
23	512	14.2	461	7	THB1_HUMAN	THYROID HORMONE RECP	6.44e-67
24	511	14.1	373	7	THB6_XENLA	THYROID HORMONE RECP	9.80e-67
25	511	14.1	414	7	THB7_XENLA	THYROID HORMONE RECP	9.80e-67
26	510	14.1	461	7	THB1_RAT	THYROID HORMONE RECP	1.49e-66
27	510	14.1	514	7	THB2_RAT	THYROID HORMONE RECP	1.49e-66
28	510	14.1	410	7	THA1_RAT	THYROID HORMONE RECP	1.49e-66
29	503	13.9	408	7	THA_CHICK	THYROID HORMONE RECP	2.82e-65
30	495	13.7	418	7	THA_RANCA	THYROID HORMONE RECP	8.07e-64
31	490	13.6	614	2	EAR1_HUMAN	V-ERBA RELATED PROTEI	6.54e-63
32	486	13.4	418	7	THAA_XENLA	THYROID HORMONE RECP	3.48e-62
33	475	13.1	418	7	THAB_XENLA	THYROID HORMONE RECP	3.48e-60
34	474	13.1	385	3	ERBA_AVIER	ERBA ONCOGENE PROTEIN	5.21e-58
35	465	12.9	455	6	RRB1_CHICK	RETINOIC ACID RECEPTO	2.21e-58
36	465	12.9	448	6	RRB2_CHICK	RETINOIC ACID RECEPTO	2.21e-58
37	464	12.8	462	6	RRB1_HUMAN	RETINOIC ACID RECEPTO	3.34e-58
38	463	12.8	462	6	RRB1_MOUSE	RETINOIC ACID RECEPTO	5.07e-58
39	463	12.8	459	6	RRB2_MOUSE	RETINOIC ACID RECEPTO	5.07e-58
40	462	12.8	458	6	RRB1_NOTVI	RETINOIC ACID RECEPTO	2.67e-57
41	459	12.7	448	6	RRB2_HUMAN	RETINOIC ACID RECEPTO	2.67e-57
42	456	12.6	455	6	RRB1_MOUSE	RETINOIC ACID RECEPTO	9.27e-57
43	456	12.6	482	6	RRB3_MOUSE	RETINOIC ACID RECEPTO	9.27e-57
44	456	12.6	448	6	RRB2_MOUSE	RETINOIC ACID RECEPTO	9.27e-57
45	455	12.6	443	6	RRG2_HUMAN	RETINOIC ACID RECEPTO	1.40e-56

ALIGNMENTS

RESULT	1
ID	PPAT_HUMAN STANDARD; PRT; 475 AA.
AC	P37231;
DT	01-OCT-1994 (REL. 30, CREATED)
DT	01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT	01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA).
GN	PPARG.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	TISSUE=LIVER;
RC	APERLO C., POGNONEC P., AUWERX J., BOULOUKOS K.J
RL	SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC	-/- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS
CC	HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
CC	THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
CC	OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROL THE
CC	PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
CC	-/- SUBCELLULAR LOCATION: NUCLEAR.
CC	-/- SUBUNIT: HETEROIMER WITH THE RETINOIC X RECEPTOR.
CC	-/- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
CC	NUCLEAR HORMONE RECEPTORS.

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US-08-380-051-2.rsp

91

Db	240	gemavtrgqlkn--gglgvvsdaifdlqvsfssfsldtdevallqvllmsedrpqlasv	297
		: : : : : : : : : : : : : : : :	
Qy	361	QGCFMTRFLKSLRKPGDFMEPKFEFAVKNALELDDSDLAIFIAVILSGDRPGLLVN	420
Db	298	eriekcqglfafehyinyrknhiafwpkllmkvtlrmigashasrflhmkecepte	357
		: : : : : : : : : : : : : :	
Qy	421	KPIEDIQNLQLAQLEQLKHNPSSQLFACKLKQKMTDLRQIVTEHV-QLLQYIKKTETD	479
Db	358	l-fppllfvfed	369
		: : : : : : : : : : : : : :	
Qy	480	MSLRPLQLQETKQ	492

Search completed: Fri Nov 17 08:30:52 1995
Job time : 15 secs.

WATERMAN

(TM)

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MPorch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Nov 17 08:31:10 1995; MacPar time 19.96 Seconds

Tabular output not generated. 590.346 Million cell updates/sec

Title: <XUS-08-380-051-2

Description: (1:494) from US08380051.pep

Perfect Score: 3614

Sequence: 1 MKLIVFLKRSAPNFTM.....KTETDMSLPLQLQYKDYLY 494

Scoring table: PAM 150
Gap 11

Searched: 78488 seqs, 23849247 residues

Database:

1 ann1
2 ann2
3 ann3
4 unann1
5 unann2
6 unann3
7 unann4
8 unann5
9 unann6
10 unann7
11 unrev1
12 unrev2

Statistics: Mean 49.868; Variance 143.995; scale 0.346

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
1	3454	95.6	505	10	A54101	peroxisome prolifera	0.00e+00	
2	3439	95.2	475	10	A49294	peroxisome prolifera	0.00e+00	
3	3433	95.0	475	10	S42489	peroxisome prolifera	0.00e+00	
4	3311	91.6	470	10	JN0881	peroxisome prolifera	0.00e+00	
5	2579	71.4	477	9	C42214	peroxisome prolifera	0.00e+00	
6	1946	53.8	468	10	A49289	peroxisome prolifera	3.90e-256	

7	1932	53.5	468	10	S11659	peroxisome prolifera	4.42e-254
8	1932	53.5	468	10	JC2085	proliferator activat	4.42e-254
9	1930	53.4	468	10	A45288	peroxisome prolifera	8.69e-254
10	1919	53.1	441	10	A45360	steroid hormone rece	3.58e-252
11	1894	52.4	474	9	A42214	peroxisome prolifera	1.66e-248
12	1743	48.2	396	9	B42214	peroxisome prolifera	2.22e-226
13	706	19.5	1237	9	A34598	ecdysone-induced pro	8.84e-77
14	672	18.6	711	12	S43464	ecdysteroid-induced	5.17e-72
15	641	17.7	1443	9	S05979	steroid hormone rece	1.11e-67
16	528	14.6	1394	9	B34598	ecdysone-induced pro	4.74e-52
17	525	14.5	373	6	C36067	thyroid hormone rece	1.22e-51
18	518	14.3	369	3	TVCHTB	thyroid hormone rece	1.11e-50
19	517	14.3	410	12	S14416	thyroid hormone rece	1.52e-50
20	517	14.3	398	6	S23614	thyroid hormone rece	1.52e-50
21	516	14.3	410	6	S26828	thyroid hormone rece	2.09e-50
22	516	14.3	410	6	A40917	thyroid hormone rece	2.09e-50
23	516	14.3	410	3	QRMSA1	thyroid hormone rece	2.09e-50
24	514	14.2	461	6	A40377	thyroid hormone rece	3.92e-50
25	514	14.2	461	6	A31820	thyroid hormone rece	3.92e-50
26	513	14.2	456	3	TVHUAR	thyroid hormone rece	5.37e-50
27	511	14.1	456	6	A31116	thyroid hormone rece	1.01e-49
28	510	14.1	410	12	S09178	thyroid hormone rece	1.38e-49
29	503	13.9	408	3	TVCHVR	thyroid hormone rece	1.38e-49
30	496	13.7	508	10	A30226	thyroid/steroid horm	1.25e-48
31	491	13.6	410	6	S06410	thyroid hormone rece	5.38e-47
32	490	13.6	614	10	A32608	thyroid hormone rece	7.36e-47
33	488	13.5	418	3	TVXLTA	thyroid hormone rece	1.38e-46
34	485	13.4	65	10	PN0676	peroxisome prolifera	3.52e-46
35	482	13.3	578	12	S52913	nuclear hormone rece	9.01e-46
36	482	13.3	461	12	JC4014	steroid hormone-nucl	9.01e-46
37	482	13.3	383	12	S52909	nuclear hormone rece	9.01e-46
38	482	13.3	533	10	JC2390	nuclear receptor Rev	9.01e-46
39	479	13.2	459	6	A41977	PML/retinoic acid re	2.30e-45
40	477	13.2	418	6	B36067	retinoic acid recept	4.30e-45
41	475	13.1	387	6	S35744	transforming protein	1.10e-44
42	474	13.1	398	3	TVFVVR	PML-1/retinoic acid	2.05e-44
43	472	13.1	398	3	TVFVVR	transforming protein	2.80e-44
44	471	13.0	398	3	TVFVVR	transforming protein	2.80e-44
45	471	13.0	398	3	TVFVVR	transforming protein	2.80e-44

ALIGNMENTS

RESULT	1
ENTRY	A54101
TITLE	peroxisome proliferator-activated receptor gamma-2 - mouse
ORGANISM	#formal_name Mus musculus #common_name house mouse
DATE	02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 02-Aug-1994
ACCESSIONS	A54101
REFERENCE	A54101
#authors	Tontonoz, P.; Hu, E.; Graves, R.A.; Budavari, A.I.;
#journal	Spiegelman, B.M.
#title	Genes Dev. (1994) 8:1224-1234
#accession	mPPARGamma2: tissue-specific regulator of an adipocyte enhancer.
#status	A54101
#molecule_type	preliminary
#residues	1-505
#cross-references	EMBL:U09138
KEYWORDS	receptor
SUMMARY	#length 505 #molecular-weight 57598 #checksum 3454

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US-08-380-051-2.rpr

3

DB 10; Score 3454; Match 97.3%; QryMatch 95.6%; Pred. No. 0.00e+00;
Matches 469; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

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Db 24 steqetmvtwptnfnfngissvdlsvmedshsfidkpfvtdfssisaphydedipf 83
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 13 SATNWTWDTWPTNFWPTNFGISSVDLSVMDHSHSFDIKPFTTVDFFSSISTPHYEDIPF 72

Db 84 tradmvdvdykldkqevsaikvepaapppyyseaktqlynrpheeppnslmaiecrvcg 143
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 73 TRDPVWADYKLDKQEVSAIKVEPASPYPYSEKTLQYNKPHEEPSNSLMAIECRVCG 132

Db 144 dksagfhgvhacegckgffrtirliklydracdlnrcrhhkksnkcqycrfqkclavgm 203
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 133 DKASGFGYVHACEGCKGFFRTIRLIKLYDRCDLNCRTHKKSNNKCQYCRFQKCLAVGM 192

Db 204 shnairfgrmpqaekekllaeissdidqlnpesadlralakhllydsyiksfpkltakara 263
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 193 SHNAIRFGRMPOAEKEKLLAEISSDIDQLNPEASADLRAKHLHYDSYIKSFPLTKAKARA 252

Db 264 iltgktdksfvdymslmggedkikfkhitplqeqskevairifqgcqfrseaveq 323
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 253 ILTKGTTDKSPFVYDMNSLWNGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSEAVEQ 312

Db 324 iteyaknipgfinldndqvllkygvheiiytmlaslmgdgvliaseqggfntreflkn 383
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 313 ITEYAKSIPGVNLNDQVTLKYGVHEIIYTMLASLWNGDGVLISEGQGFMTREFLKS 372

Db 384 lrpfgdmepkfefavkfnaleldsdlaifaviilegdrpgllnvkpiiediqnllq 443
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 373 LRPFCDMEPKFEFAVFNALELDSDLAIFAVIILSGDRPGLLNVKPIEDIQNLLQ 432

Db 444 alelqlklnhpessqlfakvlqkmtldrqivtehvlhvkiktdcmshlpollqeykd 503
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 433 ALELQLKLNHPESSQLFAKVLQKMTLDQIVTEHVQLQVKKTKETDMSLHPLLQEIYKD 492

Db 504 ly 505
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 493 LY 494

RESULT 2
ENTRY A49294 #type complete
TITLE peroxisome proliferator-activated receptor gamma - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-1995

ACCESSIONS A49294
REFERENCE A49294
#authors Zhu, Y.; Alvares, K.; Huang, Q.; Rao, M.S.; Reddy, J.K.
#journal J. Biol. Chem. (1993) 268:26817-26820
#title Cloning of a new member of the peroxisome
        proliferator-activated receptor gene family from mouse
        liver.
#accession A49294
#status preliminary
#molecule_type mRNA
#residues 1-475 #label ZHU
#cross-references CB:U01841
#length 475 #molecular-weight 54511 #checksum 6045

SUMMARY

DB 10; Score 3439; Match 98.1%; QryMatch 95.2%; Pred. No. 0.00e+00;
Matches 466; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvdtempwptnfnfngissvdlsvmedshsfidkpfvtdfssisaphydedipftradpmv 60
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4

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Qy 20 MVDTEMPWPTNFGISSVDLSVMDHSHSFDIKPFTTVDFFSSISTPHYEDIPFTRDPWV 79

Db 61 adykdyldkqevsaikvepaapppyyseaktqlynrpheeppnslmaiecrvcgdkasgh 120
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 ADYKYDYLKQEVSAIKVEPASPYPYSEKTLQYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db 121 ygvhacegckgffrtirliklydracdlnrcrhhkksnkcqycrfqkclavgmshnairf 180
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 140 YGVHACEGCKGFFRTIRLIKLYDRCDLNCRTHKKSNNKCQYCRFQKCLAVGMSHNAIRF 199

Db 181 grmpqaekekllaeissdidqlnpesadlralakhllydsyiksfpkltakaraailtkt 240
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 200 GRMPQAEKEKLLAEISSDIDQLNPEASADLRAKHLHYDSYIKSFPLTKAKARAAILTKT 259

Db 241 dkspfvdymslmggedkikfkhitplqeqskevairifqgcqfrseaveqteyaykn 300
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 260 DKSPFVYDMNSLWNGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSEAVEQTEYAKS 319

Db 301 ipgfinldndqvllkygvheiiytmlaslmgdgvliaseqggfntreflknlrpfgd 360
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 320 IPGFNLNDQVTLKYGVHEIIYTMLASLWNGDGVLISEGQGFMTREFLKSIRKPFCD 379

Db 361 fmpkfefavkfnaleldsdlaifaviilegdrpgllnvkpiiediqnllqalelqlk 420
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 380 FMPKFEFAVFNALELDSDLAIFAVIILSGDRPGLLNVKPIEDIQNLLQALELQLK 439

Db 421 lnhpessqlfakvlqkmtldrqivtehvlhvkiktdcmshlpollqeykdly 475
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 440 LNHPESSQLFAKVLQKMTLDQIVTEHVQLQVKKTKETDMSLHPLLQEIYKDL 494

RESULT 3
ENTRY S42489 #type complete
TITLE peroxisome proliferator activated receptor - human
ORGANISM #formal name Homo sapiens #common name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

ACCESSIONS S42489
REFERENCE S42489
#authors Aperlo, C.; Pognonec, P.; Auwerx, J.; Boulukos, K.
#submission submitted to the EMBL Data Library, March 1994
#description Isolation and characterization of the human peroxisome
        proliferator activated receptor, hPPARG, a member of the
        nuclear hormone receptor superfamily.
#accession S42489
#status preliminary
#molecule_type mRNA
#residues 1-475 #label APE
#cross-references EMBL:230972
#length 475 #molecular-weight 54472 #checksum 5251

SUMMARY

DB 10; Score 3433; Match 97.7%; QryMatch 95.0%; Pred. No. 0.00e+00;
Matches 464; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvdtempwptnfnfngissvdlsvmedshsfidkpfvtdfssisaphydedipftradpmv 60
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 MVDTEMPWPTNFGISSVDLSVMDHSHSFDIKPFTTVDFFSSISTPHYEDIPFTRDPWV 79

Db 61 adykdyldkqevsaikvepaapppyyseaktqlynrpheeppnslmaiecrvcgdkasgh 120
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 ADYKYDYLKQEVSAIKVEPASPYPYSEKTLQYNKPHEEPSNSLMAIECRVCGDKASGFH 139

Db 121 ygvhacegckgffrtirliklydracdlnrcrhhkksnkcqycrfqkclavgmshnairf 180
   1: 1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Qy 140 YGVHACEGCKGFFRRTRIRLKIYDRCDLNCRIHKSRNKCQYCRFOKCLAVGMSHNAIRF 199
 Db 181 grmpqaekekllaeissdldqlnpesadlralakhllydsyikspitkakarailltqkt 240
 Qy 200 GRMPQAEKEKLLAEISSDLDQLNPESEDALRALAKHLYSYIKSFP LTKAKARAILTGKTT 259
 Db 241 dkspfiydmnsfmmedekikfkhitplqeqskevairifgqcfqrsveavqeiteyagn 300
 Qy 260 DKSPFVIYDMNSFMMEDEKIKFKHITPLQEQSKEVAIRIFGQCFQRSVEAQEITEYAKS 319
 Db 301 ipgflnldndqvrtllygvheiiymtlaslmnkdvliisegqgfmreflkslrkpfqd 360
 Qy 320 IPGFVNLNDQVRTLKYGVHEIITMLASLMNKDGLVLISEGQGFMTREFLKS LRKPFQD 379
 Db 361 fmpkfefavkfnaledsdldlaifiavilsgdrpgllnvkpiiediqnllqalelqlk 420
 Qy 380 FMPKFEFAVKFNALELSDLDLAFIATVILSGDRPGLNVKPIEDIQNLLQALELQLK 439
 Db 421 lnhpessqlfakvqlqkmtldlrqvtehvqllhvikktetdmslhplqeiyykdiy 475
 Qy 440 LNPRESSQLFAKVLQKMTDLRQIVTEHVQLQVLIKKTETDMSLHP LQEIYKDIY 494

RESULT 4
 ENTRY JN0881 #type complete
 TITLE peroxisome proliferator activated receptor gamma precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 03-Mar-1995
 ACCESSIONS JN0881
 REFERENCE JN0881
 #authors Chen, F.; Law, S.W.; O'Malley, B.W.
 #journal Biochem. Biophys. Res. Commun. (1993) 196:671-677
 #title Identification of two mPPAR related receptors and evidence for the existence of five subfamily members.
 #accession JN0881
 #molecule_type mRNA
 #residues 1-470 #label CHE
 #experimental_source heart
 #superfamily erba transforming protein homology
 KEYWORDS DNA binding
 FEATURE
 1-22 #domain signal sequence #status predicted #label SIG
 23-470 #product peroxisome proliferator activated receptor gamma #status predicted #label WAT
 107-393 #domain erba transforming protein homology #label ERBA
 130-194 #region DNA-binding
 SUMMARY #length 470 #molecular_weight 54014 #checksum 9480

Db 10; Score 3311; Match 96.2%; QryMatch 91.6%; Pred. No. 0.00e+00;
 Matches 457; Conservative 11; Mismatches 2; Indels 5; Gaps 1;
 Db 1 mvdttempfwnfnfgisvdlvmedshsfidkpfittvdfsisaphyedi pfradpav 60
 Qy 20 MVDTEMFWMPTNFGISSVDLSVMEDSHSFDIKPFTTVDFSSISTPHYEDI PFRTRDPVV 79
 Db 61 adkydkllyqeqsalkvpeaspyssektqlynrphpeepsnlmaiecrvcgdkasgh 120
 Qy 80 ADKYDKLQEQSALKVPEASPPYSSEKTQLYNRPHPEEPSNLSMAIECRVC GKASGFH 139
 Db 121 ygvhacegckgffrrtrirkllydrdlnclrihkknkcqycrfqclavgmshnaif 180

Qy 140 YGVHACEGCKGFFRRTRIRLKIYDRCDLNCRIHKSRNKCQYCRFOKCLAVGMSHNAIRF 199
 Db 181 grdrqaekekllaeissdldqlnpesadlralakhllydsyikspitkakarailltqkt 240
 Qy 200 GRMPQAEKEKLLAEISSDLDQLNPESEDALRALAKHLYSYIKSFP LTKAKARAILTGKTT 259
 Db 241 dkspfiydmnsfmmedekikfkhitplqeqskevairifgqcfqrsveavqeiteyagn 300
 Qy 260 DKSPFVIYDMNSFMMEDEKIKFKHITPLQEQSKEVAIRIFGQCFQRSVEAQEITEYAKS 319
 Db 301 ipgflnldndqvrtllygvheiiymtlaslmnkdvliisegqgfmreflkslrkpfqd 360
 Qy 320 IPGFVNLNDQVRTLKYGVHEIITMLASLMNKDGLVLISEGQGFMTREFLKS LRKPFQD 379
 Db 361 fmpkfefavkfnaledsdldlaifiavilsgdrpgllnvkpiiediqnllqalelqlk 420
 Qy 380 FMPKFEFAVKFNALELSDLDLAFIATVILSGDRPGLNVKPIEDIQNLLQALELQLK 439
 Db 416 lnhpessqlfakvqlqkmtldlrqvtehvqllhvikktetdmslhplqeiyykdiy 470
 Qy 440 LNPRESSQLFAKVLQKMTDLRQIVTEHVQLQVLIKKTETDMSLHP LQEIYKDIY 494

RESULT 5
 ENTRY C42214 #type complete
 TITLE peroxisome proliferator-activated receptor gamma, xPPARgamma=nuclear hormone receptor - African clawed frog
 ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
 DATE 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
 ACCESSIONS C42214
 REFERENCE A42214
 #authors Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.; Wahli, W.
 #journal Cell (1992) 68:879-887
 #title Control of the peroxisomal beta-oxidation pathway by a novel family of nuclear hormone receptors.
 #cross-references WUID:92191267
 #accession C42214
 #status preliminary; not compared with conceptual translation
 #molecule_type nucleic acid
 #residues 1-477 #label DRE
 #cross-references NCBI:88295
 #note sequence extracted from NCBI backbone
 SUMMARY #length 477 #molecular_weight 54055 #checksum 6850

Db 9; Score 2579; Match 73.9%; QryMatch 71.4%; Pred. No. 0.00e+00;
 Matches 357; Conservative 62; Mismatches 50; Indels 14; Gaps 10;
 Db 1 mvdttempfwnfnfgisvdlvmedshsfidkpfittvdfssins-hyddildkttflc 59
 Qy 20 MVDTEMFWMPTNFGISSVDLSVMEDSHSFDIKPFTTVDFSSISTPHYEDI----PFT- 73
 Db 60 rndqspidydkllyqeqsalkvpeaspyssektqlynrphpeepsnlmaiecrvcg 118
 Qy 74 RTDPVWADYDKLQEQSALKVPEASPPYSSEKTQLYNRPHPEEPSNLSMAIECRVC 133
 Db 119 kasghygvhacegckgffrrtrirkllydrdlnclrihkknkcqycrfqclavgm 178
 Qy 134 KASGHYGVHACEGCKGFFRRTRIRLKIYDRCDLNCRIHKSRNKCQYCRFOKCLAVGMS 193
 Db 179 hnaifrgmpqaekekllaeissdldqlnpesadlralakhllydsyikspitkakapgh 238
 Qy 194 HNAIFRGMPQAEKEKLLAEISSDLDQLNPESEDALRALAKHLYSYIKSFP LTKAKARAI 253

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Db 239 pdqshrqngytrheladdggsdgavre-praeqgggdnlpal-svaltg--gvr 294
Qy 254 LTGKT-TDKSP-FVYDMSLWMGEDKIKFKHITPQEQSKEVAIRIFQCGQFRSVEAVQ 311
Db 295 eitefaknlpfvelndqvrlklygvheiiifmlaslmnkdyvlaeqgqfntreflk 354
Qy 312 EITEYAKSIPGFVNLDINDQVTLKYGVEIITYTMLASLMNKDGVLTSEGQCFMTEFLK 371
Db 355 alrkpfdfmepkfeafainseleddslafvavillegdrpgllnvkpiediqlsll 414
Qy 372 SLRKPFCDMPKPEFAVFNALDSDLAIFAVIILSGDRPCLLVKRPETIDIQNILL 431
Db 415 qalelqlnhpdaqlfakllqmdtldrqvvtqhvqlqlkkttheadmchlpilqeyk 474
Qy 432 QALELQLKLNHPSSQLFAKLQKMTDLRQIVTEHVQLQVTKTETDMSLHPLLQEIYK 491
Db 475 dly 477
Qy 492 DLY 494

RESULT 6
ENTRY A49289 #type complete
TITLE peroxisome proliferator-activated receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
07-Apr-1994
ACCESSIONS A49289
REFERENCE A49289
#authors Sher, T.; Yi, H.F.; McBride, O.W.; Gonzalez, F.J.
#journal Biochemistry (1993) 32:5598-5604
#title cDNA cloning, chromosomal mapping, and functional
characterization of the human peroxisome proliferator
activated receptor.
#accession A49289
#status preliminary
#molecule_type mRNA
#residues 1-468 ##label SHE
#cross-references CB:L02932
#note authors translated the codon AAC for residue 33 as Asp
GENETICS
#map_position 22
SUMMARY #length 468 #molecular-weight 52267 #checksum 6622
DB 10; Score 1946; Match 65.2%; QryMatch 53.8%; Pred. No. 3.90e-256;
Matches 247; Conservative 78; Mismatches 51; Indels 3; Gaps 3;
Db 92 espagal-niecricgkasyghyvhacegckgffrtirliklyvdkdsckikqknr 150
Qy 117 EEPNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRTIRLIKLYDRCDLNCRIHKSR 176
Db 151 nkcyrcrfhkclsvgmshnairfgmrpreekakaeltcchdedsetadkslakri 210
Qy 177 NKQCYCRFOKCLAVGMSHNAIRFGMRPQAEKEKLLAEI-SSDIDQINPESADIRALAKHL 235
Db 211 yeaylknfmnmkvkarvilsgkasmpfpvihdmetlmaektivakmvan-giqmkeve 269
Qy 236 YDYTKSPFLTKAKARAILTGKTTDKSPFIYDMSLWMGEDKIKFKHITPQEQSKEVA 295
Db 270 vrifhccactsvetvtefakapafanldndqvrlklygyveaifamlsvmnkdg 329
Qy 296 IRIFQCGQFRSVEAVQETEAYSIPGFVNLDINDQVTLKYGVEIITYTMLASLMNKD 355
Db 330 mliayngnfitreflknlrkpfcdimepksfakfnalelddsislfvaaliccqdrp 389
Qy 356 VLISEQCGFMTREFLKSURKPFQDFMPEKFEFAVFNALDSDLAIFAVIILSGDRP 415
Db 390 gllnigylqegivhvkllhlsqshpddtflfplklqkmvdlrlqlvtehaqlvqvik 449
Qy 416 GLLNVKRPETIDIQNILLQALELQKLNHPSSQLFAKLQKMTDLRQIVTEHVQLQVTK 475
Db 450 tesdaalhpilqeyrdmy 468
Qy 476 TETDMSLHPLLQEIYKDL 494
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Db 330 mliayngnfitreflksirkpfcdimepksfakfnalelddsislfvaaliccqdrp 389
Qy 356 VLISEQCGFMTREFLKSURKPFQDFMPEKFEFAVFNALDSDLAIFAVIILSGDRP 415
Db 390 gllnigylqegivhvkllhlsqshpddtflfplklqkmvdlrlqlvtehaqlvqvik 449
Qy 416 GLLNVKRPETIDIQNILLQALELQKLNHPSSQLFAKLQKMTDLRQIVTEHVQLQVTK 475
Db 450 tesdaalhpilqeyrdmy 468
Qy 476 TETDMSLHPLLQEIYKDL 494

RESULT 7
ENTRY S11659 #type complete
TITLE peroxisome proliferator-activated receptor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
13-Jan-1995
ACCESSIONS S11659
REFERENCE S11659
#authors Issemann, I.; Green, S.
#journal Nature (1990) 347:645-650
#title Activation of a member of the steroid hormone receptor
superfamily by peroxisome proliferators.
#cross-references M01D:91015382
#accession S11659
#status preliminary
#molecule_type mRNA
#residues 1-468 ##label ISS
SUMMARY #length 468 #molecular-weight 52432 #checksum 4196
DB 10; Score 1932; Match 64.6%; QryMatch 53.5%; Pred. No. 4.42e-254;
Matches 245; Conservative 79; Mismatches 53; Indels 2; Gaps 2;
Db 91 despgsalniecricgkasyghyvhacegckgffrtirliklyvdkdsckikqknr 150
Qy 117 EEPNSLMAIECRVCGDKASGFHYGVHACEGCKGFFRTIRLIKLYDRCDLNCRIHKSR 176
Db 151 nkcyrcrfhkclsvgmshnairfgmrpreekakaeltcchdedsetadkslgkri 210
Qy 177 NKQCYCRFOKCLAVGMSHNAIRFGMRPQAEKEKLLAEI-SSDIDQINPESADIRALAKHL 235
Db 211 heaylknfmnmkvkarvilsgktsnmpfpvihdmetlmaektivakmvangved-keae 269
Qy 236 YDYTKSPFLTKAKARAILTGKTTDKSPFIYDMSLWMGEDKIKFKHITPQEQSKEVA 295
Db 270 vrifhccqmsvetvtefakapgfandldndqvrlklygyveaifamlslnmkdg 329
Qy 296 IRIFQCGQFRSVEAVQETEAYSIPGFVNLDINDQVTLKYGVEIITYTMLASLMNKD 355
Db 330 mliayngnfitreflknlrkpfcdimepksfakfnalelddsislfvaaliccqdrp 389
Qy 356 VLISEQCGFMTREFLKSURKPFQDFMPEKFEFAVFNALDSDLAIFAVIILSGDRP 415
Db 390 gllnigylqegivhvkllhlsqshpddtflfplklqkmvdlrlqlvtehaqlvqvik 449
Qy 416 GLLNVKRPETIDIQNILLQALELQKLNHPSSQLFAKLQKMTDLRQIVTEHVQLQVTK 475
Db 450 tesdaalhpilqeyrdmy 468
Qy 476 TETDMSLHPLLQEIYKDL 494
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[illegible]

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RESULT      11
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references
#accession
#status
#molecule_type
#residues
#cross-references
#note
SUMMARY
DB 9; Score 1894; Match 64.8%; QryWatch 52.4%; Pred. No. 1.66e-248;
Matches 247; Conservative 74; Mismatches 56; Indels 4; Gaps 4;
Db 97 aedaackal-nlcrcvcdasgfhgvhacegckgffrtirlklvydcrcmckiqtk 155

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[illegible]

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Db 9; Score 1743; Match 57.9%; OryMatch 48.2%; Pred. No. 2,22e-226;
Matches 221; Conservative 79; Mismatches 80; Indels 2; Gaps 2;

Db 17 stplehgets-qsvdcckgdrasgfhgfhgacgckgffrtirmrlgyehcdnckiq 75
: | | : : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 113 NKPSHEPNSLMAIECRVGDGKSGFHYGVHACGCGKGFRTIRIKLYIDRCDLNCRIH 172
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 76 kkrnkrcycvrfnkclsqmsnhaifrgmpesekrklyqavpsdaapspvsdlvls 135
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 173 KKSRRKCYCFKQFOLGVMSHNAIRFGMPQAEKELLAETSSDIDQLNPESADLRALA 232
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Db 136 qlhssymntftmktkardilgrns-ispfvihmdmlwqaegvtwqlptqnlgt 194
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

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RESULT 15
ENTRY      S05979      #type complete
TITLE      steroid hormone receptor homolog - fruit fly (Drosophila
            melanogaster)
ALTERNATE_NAMES puff 75B protein
ORGANISM   #formal name Drosophila melanogaster
DATE       01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
            15-Oct-1994
ACCESSIONS S05979
REFERENCE  S05979
            #authors Feigl, G.; Gram, M.; Pongs, O.
            #journal Nucleic Acids Res. (1989) 17:7167-7178
            #title  A member of the steroid hormone receptor gene family is
            expressed in the 20-OH-ecdysone inducible puff 75B in
            Drosophila melanogaster.
            #cross-references MUID:90016778
            #accession S05979
            ##molecule_type mRNA
            ##residues 1-1443 ##label FEI
            ##cross-references EMBL:X15586
GENETICS
            #map_position 3 75B
            #superfamily erba transforming protein homology
            #keywords alternative splicing; DNA binding; zinc finger
FEATURE
452-727     #domain erba transforming protein homology #label ERBA
SUMMARY     #length 1443 #molecular-weight 156264 #checksum 6391

DB 9; Score 641; Match 34.2%; QryMatch 17.7%; Pred. No. 1.11e-67;
Matches 124; Conservative 88; Mismatches 126; Indels 25; Gaps 23;

Db 451 tvlcrvcgkdaagfygshcgcgkffrsiqkqiyprctknqcsilrlnrrcqc 510
Qy 125 ATECRVCGDKASGEHYGVHACEGCKGFFRTIRKLTYDRC--DLNCRIRHKSRNKQYC 182

Db 511 rllkciavmsrdavrfgrvprekarivrcnra-priaa-ssd-peppswm-tshass 566
Qy 183 RFQKCLAVGMSHNAIFRCRMPQAEKELIAETSSDIDQLNPESADLRALAKHLYDSYIKS 242

Db 567 -ppccc-ah-letceft-kek-vs-amrh-grglpstpc-htsglsaeapelqeegef- 617
Qy 243 FPLTKAKARAILTGKTDKSPFYVDNLSLMWGEDKIKFKHITPL-QEQSKEV-AIRIFQ 300

Db 618 s-q-rfahvirgvidfagmipqglltqddkftllkaglfadalvrlicmfdssinsliic 675
Qy 301 GCQFRSEAVQEITEYAKSIPGFVNLDINDQVTLKYGVEHIIYTMIASLWKKD-CVLIS 359

Db 676 lngqv-mrrdaicqanarf--lvdstfnfaermmsmltdaeiglcavlitpdrpgl 732
Qy 360 -EQGFMTRE-FKSLRKPFGEFMEKPEFAVKFNALELDSDLAIFAIVILSGDRPL 417

Db 733 rnlleiekmysrlkgclqyivagrpdpqeflakilletmpdlrtlstlhteklvvrtteh 792
Qy 418 LNVKPIEDIQDNLQALELQKLNHPESQLFAKLQKMTDLRQIVTEHVQLLIQVIRKTE 477

Db 793 kel 795
Qy 478 TDM 480
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Search completed: Fri Nov 17 08:31:34 1995
Job time : 24 secs.

CC See also R13792-R13794.

SQ Sequence 1237 AA;

DB 3; Score 680; Match 33.3%; QryMatch 18.8%; Pred. No. 1.22e-43;
Matches 120; Conservative 93; Mismatches 130; Indels 17; Gaps 15;

Db 242 tvlpvcgdkaagfhgshasegkgffrrsqkqgyrptknqcsilrlnrncqyc 301

Qy 125 AIECRVCKDASGSHYGVHACEGCKGFFRTIRIKLIYDRC--DLNCRHKKSRNKQCYC 182

Db 302 rlkkciavamsdavrfgvrkrexilaamqgst-q-nr-ggg-talatel-ddgprl 356

Qy 183 RFQKCLAVGSHNAIRFGMPQAEKEKLAETSSDIDQINPESADIRALAKHLIDSYKS 242

Db 357 la-avlahletceftkeks-amrqardcpsymptl-lacplnapelgseqefsq- 412

Qy 243 FPLTKAKARAILTKTTDKSPFVIYDMSIMMGEDKIKFKHITPLQEQSKEVAIRIFQGC 302

Db 413 pfahw--irgvidfagmpqglitqddkftllkagldalfvrlicmfdsinsicln 470

Qy 303 QFRSVEAVQETEVAKSIPGFVNLDNDQVTLKYGVEIITMLASIMNKO-GVLIS-E 360

Db 471 gqv-mrrdalqngana-gflvdstfnfaermmsmltdaeiglfaivlitpdrpgrlnl 528

Qy 361 GQGFMTREFIKSLRKPFGDFMEPKFEAFKFNALDSDLAIFAVIILSGDRPGLLNV 420

Db 529 eliekmyrslkgclviagrpdpqeflaklletmpdlrtlstlhteklvvfrtkehcl 588

Qy 421 KPIEDIQNLLQALELQIKLNHPESQIFAKLQKQWDLRQIVTEHVQLQVKKYKTTEDM 480

RESULT 4

ID P80921 standard; protein; 456 AA.

AC P80921;

DT 29-DEC-1990 (first entry)

DE Sequence encoded by human placenta thyroid receptor c-erbA cDNA

KW Hormone receptor; hormone-binding; transcription activation.

OS Homo sapiens.

PN W08803168-A.

PD 05-MAY-1988.

PF 23-OCT-1987; U02782.

PR 20-OCT-1987; US-108471.

PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;

DR WP1; 88-133242/19.

DR N-PSDB; N80918.

PT Recombinant DNA encoding hormone receptors -

PT comprising glucocorticoid, mineralocorticoid, thyroid hormone

PS Claim 17; Fig III-1(B)-1 and -2; 243pp; English.

CC DNAs encoding hormone receptors and the hormone receptors themselves are

CC claimed. The DNA can be used to make the hormone receptor proteins and

CC functional modified forms in quantities not previously possible. The

CC receptor proteins can be used to screen cpts. for receptor-agonist or

CC receptor-antagonist activity. They can also be used in diagnostic assays.

SQ Sequence 456 AA;

DB 2; Score 512; Match 31.1%; QryMatch 14.2%; Pred. No. 3.89e-30;

Matches 116; Conservative 101; Mismatches 130; Indels 26; Gaps 25;

Db 102 cvvcgdktatgyrcitcecgkgffrtitqknlhpsyckeyekvickvtrnqccerf 161

Qy 128 CRVCKDASGSHYGVHACEGCKGFFRTIR-LKLIYD-RCDLNCRIHKKSRNKQCYCR 184

Db 162 Kkciyvgmatdlv-lddsktrialkrkliee-nre-kr-rreelq-ksig-hkpeptdeee 215

Qy 185 QKCLAVGSHNAIRFGMPQAEKEKLAETSSDIDQINPESADIRALAKHLIDSYKSP 244

Db 216 liktletahvatnaqg-shw-k-qkpkfl-ped-igqapivnapegk-vdleaf-s-hf 267

Qy 245 LTKAKARAILTKTTDKSPFVIYDMSIMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQF 304

Db 268 tkiiitpairvrvdfakklpmcelpcedqiillk-gccmeimslraavrydpesetitln 326

Qy 305 -RSVE-AVOETEYAKSIPGFVNLDNDQVTLKYGVEIITMLASIM-NKDG-VLISE 360

Db 327 gemavirgqlkn--gglgvdsdaifdgmsslesfnlddtevallqavllmssdrpglacv 384

Qy 361 GQGFMTREFIKSLRKPFGDFMEPKFEAFKFNALDSDLAIFAVIILSGDRPGLLNV 420

Db 385 eriekvqdsfllafehyinyrkhvthfwpklmktvdlrmlgachasrflhmkvecepte 444

Qy 421 KPIEDIQNLLQALELQIKLNHPESQIFAKLQKQWDLRQIVTEHV-QLLQVKKYKTTED 479

Db 445 L-lpplfleved 456

Qy 480 WSLHPLLQEIYKD 492

RESULT 5

ID P80936 standard; protein; 410 AA.

AC P80936;

DT 29-DEC-1990 (first entry)

DE Sequence encode by thyroid hormone receptor cDNA from rat brain clone

DE rbeA12

KW Hormone receptor; hormone-binding; transcription activation.

OS Rat.

PN W08803168-A.

PD 05-MAY-1988.

PF 23-OCT-1987; U02782.

PR 20-OCT-1987; US-108471.

PA (SALK) Salk Inst for Biol Stud.

PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V;

DR WP1; 88-133242/19.

DR N-PSDB; N80923.

PT Recombinant DNA encoding hormone receptors -

PT comprising glucocorticoid, mineralocorticoid, thyroid hormone

PS Example; Fig VII-1(B); 243pp; English.

CC DNAs encoding hormone receptors and the hormone receptors themselves are

CC claimed. The DNA can be used to make the hormone receptor proteins and

CC functional modified forms in quantities not previously possible. The

CC receptor proteins can be used to screen cpts. for receptor-agonist or

CC receptor-antagonist activity. They can also be used in diagnostic assays.

SQ Sequence 410 AA;

DB 2; Score 510; Match 30.7%; QryMatch 14.1%; Pred. No. 5.61e-30;

Matches 115; Conservative 96; Mismatches 137; Indels 26; Gaps 25;

Db 52 qcvvcgdktatgyrcitcecgkgffrtitqknlhpsyckeyekvickvtrnqccerf 111

Qy 127 ECRVCKDASGSHYGVHACEGCKGFFRTIR-LKLIYD-RCDLNCRIHKKSRNKQCYCR 183

Db 112 fkkciavmamdlyv-lddskrvakrklieq-nrerrr-k-eem-irelqqr-eptpeew 165

Qy 184 FQKCLAVGSHNAIRFGMPQAEKEKLAETSSDIDQINPESADIRALAKHLIDSYKSF 243

Db 166 dlhiv-atehrstnaqgshw-k-qrrkfl-pdd-igqspivmmpdgdg-vdleaf-e-e 217

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Db 240 reatqrqfahftel-alvsqvaidvafaklpofqlsredqiallktksalevmilleterr 298
Qy 292 KEVAIRIF-QGQCFRSEVAQVEITEYAKSPGVNLDINDQVTLTKYGVHEIITYMTLASL 350
Db 299 ynpaseieifldksyredfaka-glqv-eifinpifefersamelqlnadaefalliais 356
Qy 351 MNKQGVLISEGQGFWM-TRE-FLKSIRKPFCDMEKFEFAVKFNALELDDSDIAIFIAVI 408
Db 357 ifsadrpnvqdlqverlqhtyvealhayvshphdrImfprmlkvlstlesvhs 416
Qy 409 ILSDRPLGNVWP FEDIQDNLQAQLQKLNHPSSQLFAKLQKMTDLQIVTEHVQ 468
Db 417 --qvalrlqdkkplplaei 435
Qy 469 LLQVIKKTETDMSLHPLQEI 489

RESULT 10

ID R27534 standard; Protein; 462 AA.
AC R27534;
DT 09-MAR-1993 (first entry)
DE RAR-alpha protein.
KW Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia;
KW APL; translocation; chromosome 17; chromosome 15; PCR; primer;
KW [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction.
OS Synthetic.
PN W09216660-A.
PD 01-OCT-1992.
PE 23-MAR-1992; U02320.
PR 22-MAR-1991; US-673838.
PR 22-MAR-1991; US-675084.
PA (SLOK) SLOAN KETERING INST CANCER.
PI Dmitrovsky E, Evans RM, Frankel S, Kazizuka A, Miller WH;
PI Warrell RP;
DR WP1; 92-349240/42.
DR N-PSDB; Q29338.
PT Marker for acute promyelocytic leukaemia and other neoplasias -
PT comprising nucleic acid and encoded abnormal retinoic acid
PT receptor-alpha receptor
PS Disclosure; Page 43-46; 84pp; English.
CC The sequence given represents the amino acid sequence of the retinoic
CC acid receptor (RAR)-alpha protein. The gene encoding this protein is
CC disrupted in a translocation of a portion of the long arm of chromosome
CC 17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)]. This
CC causes a fusion RAR-alpha and myl which is characteristic of acute
CC promyelocytic leukemia (APL). The breakpoint region has been cloned
CC and it has been shown that DNA rearrangements are clustered in the
CC region of the first intron of RAR-alpha. This sequence was isolated
CC by polymerase chain reaction (PCR). The primers used for amplification
CC of this sequence can also be used to amplify the translocated region.
SQ Sequence 462 AA;

DB 5; Score 464; Match 33.4%; Qcymatch 12.8%; Pred. No. 2.53e-26;
Matches 122; Conservative 91; Mismatches 110; Indels 42; Gaps 23;

Db 88 cfvcdkssgyhygvsaceqgffrrisqikmvyvchrdnkciinkvtrncqycriqk 147
Qy 128 CAVGCDKASGFHYGVHACGCGGFFRTIRILYD-RCDJANCRIHKKSRNKQCYCFQK 186
Db 148 cfeygmakesvnrdr-nkktkevtpke-cseaytltpevgel-iek-vrkahqetfp-- 200
Qy 187 CLAVGMSHNAIRFGMPQAEKEKLEIISDDIQINPESADLRALAKHLYDSYKSFPLT 246

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12

Db 201 -alcq--l-gk-----ytt-n-n-s---segrvsl-did-lwdkfselstk---c-i-- 236
Qy 247 KAKARAILTKGTTKDSKSPFVIYDANSIMWGEDKIKFKHITPLOGESKEVAIRIFGQCQFRS 306
Db 237 iktv-----efakqlpofitltiadqitllkaacdililriactrytpeqdmfstdqilt- 291
Qy 307 VEAVQVEITEYAKSPGVNLDINDQVTLTKYGVHEIITYMTL-ASLM-NKDGVLISEGQGF 364
Db 292 lnrntqmbha--qfgpltdlvfafanqlpllemdaetgllsaiclicqdrdqleqpdrvd 349
Qy 365 MTRFEIKSLRKPFCDMEKFEFAVKFNALELDDSDIAIFIAVILSGDRPGLNVRKPIE 424
Db 350 mlqepallealkvyvkrprphmfpmkmitdlsrsakgaervitlkm-eipgsmpv 408
Qy 425 DIQDNLQAQLQKLNHPSSQLFAKLQKMTDLQIVTEHVQILQVKKTKETDMSLAP 484
Db 409 liqem 413
Qy 485 LIAQEI 489

RESULT 11

ID R10547 standard; protein; 462 AA.
AC R10547;
DT 11-APR-1991 (first entry)
DE Murine Retinoic Acid Receptor-alpha (deduced from cDNA).
KW mouse; retinoic acid receptor; mRAR-alpha; embryogenesis.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 1..59
FT /label= Region A
FT /note= "important for differential trans-activa-
FT tion by other nuclear receptors"
FT Region 60..87
FT /label= Region B
FT /note= "well conserved between mRAR's"
FT Region 88..153
FT /label= Region C
FT /note= "DNA binding domain. 95 per cent amino acid
FT identity between mRAR's"
FT Region 154..199
FT /label= Region D
FT /note= "putative hinge region"
FT Region 200..419
FT /label= Region E
FT /note= "ligand binding domain"
FT Region 420..462
FT /label= Region F
PN EP-411323-A.
PD 06-FEB-1991.
PD 29-JUN-1990; 112469.
PR 30-JUN-1989; US-374690.
PR 29-MAR-1990; US-502140.
PA (INRM) INSERM INST NAT SANTE.
PA (SQUI) LES LABS SQUIBB SA.
PI Chambon P, Kastner P, Krust A, Petkovich M, Zelent A;
PI Leroy P, Mendelsohn C, Staub A;
DR WP1; 91-038271/06.
PT Novel human and mouse retinoic acid receptors - encode proteins
PT used to assay for agonists and antagonists
PS Disclosure; Fig 1; 33pp; English.
CC An 11.5 day-old total mouse embryo lambda gt10 cDNA library was
CC screened with labelled human RAR-alpha probes. Positive clones were
CC isolated, mapped and sequenced. A set of mRAR-alpha clones was

Search completed: Fri Nov 17 08:32:06 1995
Job time : 15 secs.